SEQUENCE LISTING

<110> Smith, John Craig

<120> DIAGNOSTIC METHOD

<130> 06275-276002

<140> US 10/621,116
<141> 2003-07-16

<150> US 09/778,900
<151> 2001-02-08

<150> GB 0004232.5
<151> 2000-02-24

<160> 27

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 1073
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(1073)
<223> n = A,T,C or G

<400> 1
gggtttactt tgccacttct tgcttttcct atatatgtag aaaagccaca gtgcgcccca 60
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ttagtcattg tttggaatga ctttataaaa atgctttgca ttttttagca agaccatcat 180
ataattgttt aagatcaagt acaacacata aggtcactgg agaatttgag tgcatgttat 240
ccaagatagg atggtagagc tcacattaca gaaatgtagt gtgggaatag taaggagtcg 300
tttaatagaa attgcacacc taagtgtgat gagtgtatgt gaatgtggag aagtactttc 360
tgcacctggc cacacagttt caaccaaatg atcccnaaat aaaacagtgg atgttaacgg 420
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agtcttcttc tgaaataaag actgactacc tatcaattat aatggaccca gatgaagttc 540
ctttggatga gcagtgtgag cggctccctt atgatgccag caagtgggag tttgcccggg 600
agagacttaa actgggtaag atatttgttc aacagattca taaacctata ctgagcacat 660
attacatgaa aaacactgtg ctttgagaga tgcgaaagta aactagacct gggattctac 720
cctccagctg ctcacagact agcaagggag atggacacaa aagtaaataa ttccaatgca 780
atgctcagat aacagtacaa ggtgacacgc agcacctgtt tgttcttgca acagttatta 840
ggcaccttct ctgagcagca gacactggtc taagccctgg agacacaaag gtgcttgcat 900
ctcttccctc aaagggctca gtctggagat aggtgcaaaa gtggtaagtg aaggggggcg 960
gagagagagg cattacaagt acacgcacgc ttcataatga aactgttgag ggattagaaa 1020
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<210> 2
<211> 1480
<212> DNA
<213> Homo sapiens

<220>
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<222> (1)...(1480)
<223> n = A,T,C or G

<400> 2
cactgtgccc ggccagcttt gctatttatt agctgcatgt gaatttgatt actttacttc 60
tctgaacctg tttctccatg tataaataag aactacttcg taaaattgtt ggaaacacta 120
aacaagaaat gnacctaaag cttttaatat accagctcac acagagtaag cattcagtaa 180
atacccacca ctcttaattt tttttttta tctgatctaa gatgctgtct agaagcccag 240
gcaagagcac aatagactct gcaactccag aggtagtcag gctcctggac accgtagggc 300
ccctgtgcta gttcacgatc cattttgaga agtgaaacgc tctcatttct catcaggcna 360
ttgccagttg agggactggt ttcccnctgc tgtgctggag ctccttttca cctgggtcct 420
tttcggtctc ttcaaaggat gcagcactac acatggagcc taagaaagaa aaaatggagc 480
caggcctgga acaaggcaag aaaccaagac tagatagcgt caccagcagc gaaagctttg 540
cgagctccgg ctttcaggaa gataaaagtc tgagtgatgt tgaggaagag gagggtaggt 600
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accgttttct cccctcaggg attttcatct taatggatca tccccctgcc cccatgcttg 840
gataaagtgg gctggaggcc tggaaaaatc tctggtgttc atgttgaaac tcaaatactc 900
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ccttgatatg aggagttttg agaatgagga gtcatggata ccagtggata gaacttaatt 1320
ctggggaaaa ctcacaggtt tcagactaga caaacctggc atcggctctc cacagtatcc 1380
tctggcatat tttcaaatct ggcccaaatc tcagaagaca tgacttcata ggagagctac 1440
tattaatata gccatatagg gccctcccac aaaactgcag 1480

<210> 3
<211> 726
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(726)
<223> n = A,T,C or G

<400> 3
cagagctatg cagataagga catgctgaac acatcagagg ggcttactga acatatacng 60
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ggtgttctct atgttaggaa accagagctg ctctcggaaa tgatttatag gccgtatgtt 180
atctgggagg tgaccccatg gacactcggg ttgaatgtgc tttgttttca tgcccttctg 240
ctcaaggccc ccttgccctc ttctagactc gacttcctct gaaatggatg gctcctgaat 300
ctatctttga caaaatctac agcaccaaga gcgacgtgtg gtcttacgga gtattgctgt 360
gggaaatctt ctccttaggt aaatttggga gaaggaagaa atcaaacagc ccagaaataa 420
atgtctgcat cttctgctga atgtcctttg gttggacagc ctttagatta gaacctactg 480
taacaaaaaa ctcttaaagt gtaatgggcc catgtagact ctcagatgag taatggcgta 540
cgcatgtctg ccctctactg taaaagggct ttatatgatc atgaacaagg tcagaacaag 600
gtcatgtaaa agggctttat acgatcatga acaagggtat aaagtctgaa gcaaagtact 660
ttttctgtac tttgccaatt ctgccttttc aattcctcaa cacccacacc tctaatgccc 720
ttaccg 726

<210> 4
<211> 1352
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(1352)
<223> n = A,T,C or G

<400> 4
ctgcagaggc cacaggcaca acaaagaacc tgggtatcca tgagctctgg tgggttggtt 60
agtctgcctt ggtagacgtg ttttccactg accacaggac ctggcccaga cagcctttta 120
agtgctggtg ctataaaccc aaacctaaaa atgaagcagg gtcacatagt acagaaagct 180
tgggctttat gcggatgatg acagccctcc ctttgtagta cgtaaggcaa tgcataggat 240
gatcactgct ctccaactat ttctgttgct gttttcccca ccagctatca gatcatgctg 300
gactgctggc acagagaccc aaaagaaagg ccaagatttg cagaacttgt ggaaaaacta 360
ggtgatttgc ttcaagcaaa tgtacaacag gtaaaactaa atttatctac atcaaaatgc 420
ctttgaatgt acgtcagggg ggcattttat ttgtttttt tttaagagct attaatataa 480
tagctgagat cagaagttta aaaaaagggt gtgtgtgtgt gtatacagaa ttatcttctc 540
aaaacacaac caagattgtg gcaaatgaca tagtcaaagt tgacataatg gttcatagaa 600
attgttgaag tcagaattgg tgcaacgaga gctctacctt tggtatttta ggatggtaaa 660
gactacatcc caatcaatgc catactgaca ggaaatagtg ggtttacata ctcaactcct 720
gccttctctg aggacttctt caaggaaagt atttcagctc cgaagtttaa ttcaggaagc 780
tctgatgatg tcaggtaaga tttctttctc aaactttata tcacagaatt ttccaacaaa 840
aaaaagaaag aaagaaagac gaaagagaaa gaaagacnga aagagagaaa gaaagagaga 900
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tggctcgtgc ctgtaatcgc agcactttgg gagactgagg tgggaggatc acttgagcct 1200
aggagttcaa aatctgcctc ggcaacatag agagacctca tcttactaaa aatttaaaaa 1260
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<210> 5
<211> 1256
<212> DNA
<213> Homo sapiens

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tagagacatc atacaacact acccaattct tcccaatctg taatcacaca cacacacaaa 120
atacaagcct ggcactagca ctcgattatg ccattaaata atatttagcc gtgtagccat 180
gccaggtcac tttgccacct cacatccttt tcagagcacc tgataaagtc ataccacttc 240
cctgcacatc atttctctcc tgtgccattg ggcactcaga cgagatgatg cctccagtct 300
ctcctacgtc tggcattctc tgatttcaca acggaccaga gtaggtccct ctgggagttt 360
cctcaaccct acagaatgtg aattgacaac cacgggaggc agtggcaatg ctgtcaggat 420
tcccaggggt cacggcgggg agatcggggc ctcaggagtt aggtgattcc tgttggtgtg 480
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tgatgtaagt cgtgaagtta aggtacctag tgcactccga tagacccctt cttcagatcc 720
cttccaaaca ccaacgccag taatgtagta gttcttggtc agtgagggtc tggattcagg 780
agtggctgaa atgacagtgt ggggaggact gacaactaga cctagctgtg cagaactaat 840
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gaccctgagg aaactccatt gtgtgtttct aagctgctta gctgtcagtg atgcagcttt 960
gctttcagag taacagagga actcccagct gtgtgggtga tgggctttgt gatgtaacag 1020
agagcgcgtt cctgcaagca gccttgaggc tgggaggggt ccacctaagc cttatgctcc 1080
tttcccctga ggttctacag attgaacagc tgtgttccta cccaatcaca atgggagaag 1140
ctaaccagta tagcctggca aacaagaggt cttccagctc ttctctctaa agccctgtga 1200
tgtggggttg aggggctaag gggaggagag gagcatgggc aggagcgata ctgcag 1256

<210> 6
<211> 31
<212> DNA
<213> Homo sapiens

<400> 6
ggaaaaaatg ccgacrgaag gagaggacct g 31

<210> 7
<211> 31
<212> DNA
<213> Homo sapiens

<400> 7
gaaatggatg gctccygaat ctatctttga c 31

<210> 8
<211> 31
<212> DNA
<213> Homo sapiens

<400> 8
tgatgatgtc agataygtaa atgctttcaa g 31

<210> 9
<211> 31
<212> DNA
<213> Homo sapiens

<400> 9
aaaaagacac ggacaygctc ccctgggacc t 31

<210> 10
<211> 31
<212> DNA
<213> Homo sapiens

<400> 10
gatcggactt tccgcyccta gggccaggcg g 31

<210> 11
<211> 31
<212> DNA
<213> Homo sapiens

<400> 11
gacggactct ggcggycggg tctttggccg c 31

<210> 12
<211> 31

<212> DNA
<213> Homo sapiens

<400> 12
tctggcggcc gggtckttgg ccgcggggag c 31

<210> 13
<211> 31
<212> DNA
<213> Homo sapiens

<400> 13
gaatgtcctt tggttrgaca gcctttagat t 31

<210> 14
<211> 31
<212> DNA
<213> Homo sapiens

<400> 14
aggtacctag tgcacyccga tagacccctt c 31

<210> 15
<211> 34
<212> DNA
<213> Homo sapiens

<400> 15
atgggtttca tgttaacttg gaaaaaatgc gtac 34

<210> 16
<211> 28
<212> DNA
<213> Homo sapiens

<400> 16
cattcatgat ggtaagatta agagtgat 28

<210> 17
<211> 35
<212> DNA
<213> Homo sapiens

<400> 17
tcttggttgc tgtagatttt gtcaaagata gctgc 35

<210> 18
<211> 24
<212> DNA
<213> Homo sapiens

<400> 18
accccatgga cactcgggtt gaat 24

<210> 19
<211> 25
<212> DNA

<213> Homo sapiens

<400> 19
cctcaaccct acagaatgtg aattg 25

<210> 20
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<400> 20
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<210> 21
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<210> 22
<211> 18
<212> DNA
<213> Homo sapiens

<400> 22
gtgttcttgg cacggagg 18

<210> 23
<211> 35
<212> DNA
<213> Homo sapiens

<400> 23
ggcgcggcca gcttcccttg gatcggactt ggcgc 35

<210> 24
<211> 34
<212> DNA
<213> Homo sapiens

<400> 24
ctgctcgccc ggtgcccgcg ctccccgcgg ttaa 34

<210> 25
<211> 7680
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (250)...(4266)

<400> 25
gcggacactc ctctcggctc ctccccggca gcggcggcgg ctcggagcgg gctccggggc 60
tcgggtgcag cggccagcgg gcctggcggc gaggattacc cggggaagtg gttgtctcct 120

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ggctggagcc gcgagacggg cgctcagggc gcggggccgg cggcggcgaa cgagaggacg    180
gactctggcg gccgggtcgt tggccggggg agcgcgggca ccgggcgagc aggccgcgtc    240
gcgctcacc atg gtc agc tac tgg gac acc ggg gtc ctg ctg tgc gcg ctg    291
          Met Val Ser Tyr Trp Asp Thr Gly Val Leu Leu Cys Ala Leu
           1               5                  10

ctc agc tgt ctg ctt ctc aca gga tct agt tca ggt tca aaa tta aaa      339
Leu Ser Cys Leu Leu Leu Thr Gly Ser Ser Ser Gly Ser Lys Leu Lys
 15                  20                  25                  30

gat cct gaa ctg agt tta aaa ggc acc cag cac atc atg caa gca ggc      387
Asp Pro Glu Leu Ser Leu Lys Gly Thr Gln His Ile Met Gln Ala Gly
                35                  40                  45

cag aca ctg cat ctc caa tgc agg ggg gaa gca gcc cat aaa tgg tct      435
Gln Thr Leu His Leu Gln Cys Arg Gly Glu Ala Ala His Lys Trp Ser
            50                  55                  60

ttg cct gaa atg gtg agt aag gaa agc gaa agg ctg agc ata act aaa      483
Leu Pro Glu Met Val Ser Lys Glu Ser Glu Arg Leu Ser Ile Thr Lys
        65                  70                  75

tct gcc tgt gga aga aat ggc aaa caa ttc tgc agt act tta acc ttg      531
Ser Ala Cys Gly Arg Asn Gly Lys Gln Phe Cys Ser Thr Leu Thr Leu
    80                  85                  90

aac aca gct caa gca aac cac act ggc ttc tac agc tgc aaa tat cta      579
Asn Thr Ala Gln Ala Asn His Thr Gly Phe Tyr Ser Cys Lys Tyr Leu
 95                  100                 105                 110

gct gta cct act tca aag aag aag gaa aca gaa tct gca atc tat ata      627
Ala Val Pro Thr Ser Lys Lys Lys Glu Thr Glu Ser Ala Ile Tyr Ile
                115                 120                 125

ttt att agt gat aca ggt aga cct ttc gta gag atg tac agt gaa atc      675
Phe Ile Ser Asp Thr Gly Arg Pro Phe Val Glu Met Tyr Ser Glu Ile
            130                 135                 140

ccc gaa att ata cac atg act gaa gga agg gag ctc gtc att ccc tgc      723
Pro Glu Ile Ile His Met Thr Glu Gly Arg Glu Leu Val Ile Pro Cys
        145                 150                 155

cgg gtt acg tca cct aac atc act gtt act tta aaa aag ttt cca ctt      771
Arg Val Thr Ser Pro Asn Ile Thr Val Thr Leu Lys Lys Phe Pro Leu
    160                 165                 170

gac act ttg atc cct gat gga aaa cgc ata atc tgg gac agt aga aag      819
Asp Thr Leu Ile Pro Asp Gly Lys Arg Ile Ile Trp Asp Ser Arg Lys
175                 180                 185                 190

ggc ttc atc ata tca aat gca acg tac aaa gaa ata ggg ctt ctg acc      867
Gly Phe Ile Ile Ser Asn Ala Thr Tyr Lys Glu Ile Gly Leu Leu Thr
                195                 200                 205

tgt gaa gca aca gtc aat ggg cat ttg tat aag aca aac tat ctc aca      915
Cys Glu Ala Thr Val Asn Gly His Leu Tyr Lys Thr Asn Tyr Leu Thr
            210                 215                 220
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cat cga caa acc aat aca atc ata gat gtc caa ata agc aca cca cgc      963
His Arg Gln Thr Asn Thr Ile Ile Asp Val Gln Ile Ser Thr Pro Arg
        225                 230                 235

cca gtc aaa tta ctt aga ggc cat act ctt gtc ctc aat tgt act gct     1011
Pro Val Lys Leu Leu Arg Gly His Thr Leu Val Leu Asn Cys Thr Ala
    240                 245                 250

acc act ccc ttg àac acg aga gtt caa atg acc tgg agt tac cct gat     1059
Thr Thr Pro Leu Asn Thr Arg Val Gln Met Thr Trp Ser Tyr Pro Asp
255                 260                 265                 270

gaa aaa aat aag aga gct tcc gta agg cga cga att gac caa agc aat     1107
Glu Lys Asn Lys Arg Ala Ser Val Arg Arg Arg Ile Asp Gln Ser Asn
                275                 280                 285

tcc cat gcc aac ata ttc tac agt gtt ctt act att gac aaa atg cag     1155
Ser His Ala Asn Ile Phe Tyr Ser Val Leu Thr Ile Asp Lys Met Gln
            290                 295                 300

aac aaa gac aaa gga ctt tat act tgt cgt gta agg agt gga cca tca     1203
Asn Lys Asp Lys Gly Leu Tyr Thr Cys Arg Val Arg Ser Gly Pro Ser
        305                 310                 315

ttc aaa tct gtt aac acc tca gtg cat ata tat gat aaa gca ttc atc     1251
Phe Lys Ser Val Asn Thr Ser Val His Ile Tyr Asp Lys Ala Phe Ile
    320                 325                 330

act gtg aaa cat cga aaa cag cag gtg ctt gaa acc gta gct ggc aag     1299
Thr Val Lys His Arg Lys Gln Gln Val Leu Glu Thr Val Ala Gly Lys
335                 340                 345                 350

cgg tct tac cgg ctc tct atg aaa gtg aag gca ttt ccc tcg ccg gaa     1347
Arg Ser Tyr Arg Leu Ser Met Lys Val Lys Ala Phe Pro Ser Pro Glu
                355                 360                 365

gtt gta tgg tta aaa gat ggg tta cct gcg act gag aaa tct gct cgc     1395
Val Val Trp Leu Lys Asp Gly Leu Pro Ala Thr Glu Lys Ser Ala Arg
            370                 375                 380

tat ttg act cgt ggc tac tcg tta att atc aag gac gta act gaa gag     1443
Tyr Leu Thr Arg Gly Tyr Ser Leu Ile Ile Lys Asp Val Thr Glu Glu
        385                 390                 395

gat gca ggg aat tat aca atc ttg ctg agc ata aaa cag tca aat gtg     1491
Asp Ala Gly Asn Tyr Thr Ile Leu Leu Ser Ile Lys Gln Ser Asn Val
    400                 405                 410

ttt aaa aac ctc act gcc act cta att gtc aat gtg aaa ccc cag att     1539
Phe Lys Asn Leu Thr Ala Thr Leu Ile Val Asn Val Lys Pro Gln Ile
415                 420                 425                 430

tac gaa aag gcc gtg tca tcg ttt cca gac ccg gct ctc tac cca ctg     1587
Tyr Glu Lys Ala Val Ser Ser Phe Pro Asp Pro Ala Leu Tyr Pro Leu
                435                 440                 445
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ggc agc aga caa atc ctg act tgt acc gca tat ggt atc cct caa cct     1635
Gly Ser Arg Gln Ile Leu Thr Cys Thr Ala Tyr Gly Ile Pro Gln Pro
            450                 455                 460

aca atc aag tgg ttc tgg cac ccc tgt aac cat aat cat tcc gaa gca     1683
Thr Ile Lys Trp Phe Trp His Pro Cys Asn His Asn His Ser Glu Ala
        465                 470                 475

agg tgt gac ttt tgt tcc aat aat gaa gag tcc ttt atc ctg gat gct     1731
Arg Cys Asp Phe Cys Ser Asn Asn Glu Glu Ser Phe Ile Leu Asp Ala
    480                 485                 490

gac agc aac atg gga aac aga att gag agc atc act cag cgc atg gca     1779
Asp Ser Asn Met Gly Asn Arg Ile Glu Ser Ile Thr Gln Arg Met Ala
495                 500                 505                 510

ata ata gaa gga aag aat aag atg gct agc acc ttg gtt gtg gct gac     1827
Ile Ile Glu Gly Lys Asn Lys Met Ala Ser Thr Leu Val Val Ala Asp
                515                 520                 525

tct aga att tct gga atc tac att tgc ata gct tcc aat aaa gtt ggg     1875
Ser Arg Ile Ser Gly Ile Tyr Ile Cys Ile Ala Ser Asn Lys Val Gly
            530                 535                 540

act gtg gga aga aac ata agc ttt tat atc aca gat gtg cca aat ggg     1923
Thr Val Gly Arg Asn Ile Ser Phe Tyr Ile Thr Asp Val Pro Asn Gly
        545                 550                 555

ttt cat gtt aac ttg gaa aaa atg ccg acg gaa gga gag gac ctg aaa     1971
Phe His Val Asn Leu Glu Lys Met Pro Thr Glu Gly Glu Asp Leu Lys
    560                 565                 570

ctg tct tgc aca gtt aac aag ttc tta tac aga gac gtt act tgg att     2019
Leu Ser Cys Thr Val Asn Lys Phe Leu Tyr Arg Asp Val Thr Trp Ile
575                 580                 585                 590

tta ctg cgg aca gtt aat aac aga aca atg cac tac agt att agc aag     2067
Leu Leu Arg Thr Val Asn Asn Arg Thr Met His Tyr Ser Ile Ser Lys
                595                 600                 605

caa aaa atg gcc atc act aag gag cac tcc atc act ctt aat ctt acc     2115
Gln Lys Met Ala Ile Thr Lys Glu His Ser Ile Thr Leu Asn Leu Thr
            610                 615                 620

atc atg aat gtt tcc ctg caa gat tca ggc acc tat gcc tgc aga gcc     2163
Ile Met Asn Val Ser Leu Gln Asp Ser Gly Thr Tyr Ala Cys Arg Ala
        625                 630                 635

agg aat gta tac aca ggg gaa gaa atc ctc cag aag aaa gaa att aca     2211
Arg Asn Val Tyr Thr Gly Glu Glu Ile Leu Gln Lys Lys Glu Ile Thr
    640                 645                 650

atc aga gat cag gaa gca cca tac ctc ctg cga aac ctc agt gat cac     2259
Ile Arg Asp Gln Glu Ala Pro Tyr Leu Leu Arg Asn Leu Ser Asp His
655                 660                 665                 670

aca gtg gcc atc agc agt tcc acc act tta gac tgt cat gct aat ggt     2307
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Thr Val Ala Ile Ser Ser Ser Thr Thr Leu Asp Cys His Ala Asn Gly
                675                 680                 685

gtc ccc gag cct cag atc act tgg ttt aaa aac aac cac aaa ata caa      2355
Val Pro Glu Pro Gln Ile Thr Trp Phe Lys Asn Asn His Lys Ile Gln
            690                 695                 700

caa gag cct gga att att tta gga cca gga agc agc acg ctg ttt att      2403
Gln Glu Pro Gly Ile Ile Leu Gly Pro Gly Ser Ser Thr Leu Phe Ile
        705                 710                 715

gaa aga gtc aca gaa gag gat gaa ggt gtc tat cac tgc aaa gcc acc      2451
Glu Arg Val Thr Glu Glu Asp Glu Gly Val Tyr His Cys Lys Ala Thr
    720                 725                 730

aac cag aag ggc tct gtg gaa agt tca gca tac ctc act gtt caa gga      2499
Asn Gln Lys Gly Ser Val Glu Ser Ser Ala Tyr Leu Thr Val Gln Gly
735                 740                 745                 750

acc tcg gac aag tct aat ctg gag ctg atc act cta aca tgc acc tgt      2547
Thr Ser Asp Lys Ser Asn Leu Glu Leu Ile Thr Leu Thr Cys Thr Cys
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gtg gct gcg act ctc ttc tgg ctc cta tta acc ctc ctt atc cga aaa      2595
Val Ala Ala Thr Leu Phe Trp Leu Leu Leu Thr Leu Leu Ile Arg Lys
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atg aaa agg tct tct tct gaa ata aag act gac tac cta tca att ata      2643
Met Lys Arg Ser Ser Ser Glu Ile Lys Thr Asp Tyr Leu Ser Ile Ile
        785                 790                 795

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Met Asp Pro Asp Glu Val Pro Leu Asp Glu Gln Cys Glu Arg Leu Pro
    800                 805                 810

tat gat gcc agc aag tgg gag ttt gcc cgg gag aga ctt aaa ctg ggc      2739
Tyr Asp Ala Ser Lys Trp Glu Phe Ala Arg Glu Arg Leu Lys Leu Gly
815                 820                 825                 830

aaa tca ctt gga aga ggg gct ttt gga aaa gtg gtt caa gca tca gca      2787
Lys Ser Leu Gly Arg Gly Ala Phe Gly Lys Val Val Gln Ala Ser Ala
                835                 840                 845

ttt ggc att aag aaa tca cct acg tgc cgg act gtg gct gtg aaa atg      2835
Phe Gly Ile Lys Lys Ser Pro Thr Cys Arg Thr Val Ala Val Lys Met
            850                 855                 860

ctg aaa gag ggg gcc acg gcc agc gag tac aaa gct ctg atg act gag      2883
Leu Lys Glu Gly Ala Thr Ala Ser Glu Tyr Lys Ala Leu Met Thr Glu
        865                 870                 875

cta aaa atc ttg acc cac att ggc cac cat ctg aac gtg gtt aac ctg      2931
Leu Lys Ile Leu Thr His Ile Gly His His Leu Asn Val Val Asn Leu
    880                 885                 890

ctg gga gcc tgc acc aag caa gga ggg cct ctg atg gtg att gtt gaa      2979
Leu Gly Ala Cys Thr Lys Gln Gly Gly Pro Leu Met Val Ile Val Glu
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Tyr Cys Lys Tyr Gly Asn Leu Ser Asn Tyr Leu Lys Ser Lys Arg Asp
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tta ttt ttt ctc aac aag gat gca gca cta cac atg gag cct aag aaa     3075
Leu Phe Phe Leu Asn Lys Asp Ala Ala Leu His Met Glu Pro Lys Lys
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gaa aaa atg gag cca ggc ctg gaa caa ggc aag aaa cca aga cta gat     3123
Glu Lys Met Glu Pro Gly Leu Glu Gln Gly Lys Lys Pro Arg Leu Asp
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agc gtc acc agc agc gaa agc ttt gcg agc tcc ggc ttt cag gaa gat     3171
Ser Val Thr Ser Ser Glu Ser Phe Ala Ser Ser Gly Phe Gln Glu Asp
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aaa agt ctg agt gat gtt gag gaa gag gag gat tct gac ggt ttc tac     3219
Lys Ser Leu Ser Asp Val Glu Glu Glu Glu Asp Ser Asp Gly Phe Tyr
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aag gag ccc atc act atg gaa gat ctg att tct tac agt ttt caa gtg     3267
Lys Glu Pro Ile Thr Met Glu Asp Leu Ile Ser Tyr Ser Phe Gln Val
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gcc aga ggc atg gag ttc ctg tct tcc aga aag tgc att cat cgg gac     3315
Ala Arg Gly Met Glu Phe Leu Ser Ser Arg Lys Cys Ile His Arg Asp
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ctg gca gcg aga aac att ctt tta tct gag aac aac gtg gtg aag att     3363
Leu Ala Ala Arg Asn Ile Leu Leu Ser Glu Asn Asn Val Val Lys Ile
        1025                1030                1035

tgt gat ttt ggc ctt gcc cgg gat att tat aag aac ccc gat tat gtg     3411
Cys Asp Phe Gly Leu Ala Arg Asp Ile Tyr Lys Asn Pro Asp Tyr Val
    1040                1045                1050

aga aaa gga gat act cga ctt cct ctg aaa tgg atg gct ccc gaa tct     3459
Arg Lys Gly Asp Thr Arg Leu Pro Leu Lys Trp Met Ala Pro Glu Ser
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atc ttt gac aaa atc tac agc acc aag agc gac gtg tgg tct tac gga     3507
Ile Phe Asp Lys Ile Tyr Ser Thr Lys Ser Asp Val Trp Ser Tyr Gly
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gta ttg ctg tgg gaa atc ttc tcc tta ggt ggg tct cca tac cca gga     3555
Val Leu Leu Trp Glu Ile Phe Ser Leu Gly Gly Ser Pro Tyr Pro Gly
            1090                1095                1100

gta caa atg gat gag gac ttt tgc agt cgc ctg agg gaa ggc atg agg     3603
Val Gln Met Asp Glu Asp Phe Cys Ser Arg Leu Arg Glu Gly Met Arg
        1105                1110                1115

atg aga gct cct gag tac tct act cct gaa atc tat cag atc atg ctg     3651
Met Arg Ala Pro Glu Tyr Ser Thr Pro Glu Ile Tyr Gln Ile Met Leu
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Asp Cys Trp His Arg Asp Pro Lys Glu Arg Pro Arg Phe Ala Glu Leu
1135                1140                1145                1150

gtg gaa aaa cta ggt gat ttg ctt caa gca aat gta caa cag gat ggt     3747
Val Glu Lys Leu Gly Asp Leu Leu Gln Ala Asn Val Gln Gln Asp Gly
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aaa gac tac atc cca atc aat gcc ata ctg aca gga aat agt ggg ttt     3795
Lys Asp Tyr Ile Pro Ile Asn Ala Ile Leu Thr Gly Asn Ser Gly Phe
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Thr Tyr Ser Thr Pro Ala Phe Ser Glu Asp Phe Phe Lys Glu Ser Ile
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Ser Ala Pro Lys Phe Asn Ser Gly Ser Ser Asp Asp Val Arg Tyr Val
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Asn Ala Phe Lys Phe Met Ser Leu Glu Arg Ile Lys Thr Phe Glu Glu
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ctt tta ccg aat gcc acc tcc atg ttt gat gac tac cag ggc gac agc     3987
Leu Leu Pro Asn Ala Thr Ser Met Phe Asp Asp Tyr Gln Gly Asp Ser
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Ser Thr Leu Leu Ala Ser Pro Met Leu Lys Arg Phe Thr Trp Thr Asp
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agc aaa ccc aag gcc tcg ctc aag att gac ttg aga gta acc agt aaa     4083
Ser Lys Pro Lys Ala Ser Leu Lys Ile Asp Leu Arg Val Thr Ser Lys
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Ser Lys Glu Ser Gly Leu Ser Asp Val Ser Arg Pro Ser Phe Cys His
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tcc agc tgt ggg cac gtc agc gaa ggc aag cgc agg ttc acc tac gac     4179
Ser Ser Cys Gly His Val Ser Glu Gly Lys Arg Arg Phe Thr Tyr Asp
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cac gct gag ctg gaa agg aaa atc gcg tgc tgc tcc ccg ccc cca gac     4227
His Ala Glu Leu Glu Arg Lys Ile Ala Cys Cys Ser Pro Pro Pro Asp
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Tyr Asn Ser Val Val Leu Tyr Ser Thr Pro Pro Ile  *
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Glu Leu Ser Leu Lys Gly Thr Gln His Ile Met Gln Ala Gly Gln Thr
        35                  40                  45
Leu His Leu Gln Cys Arg Gly Glu Ala Ala His Lys Trp Ser Leu Pro
    50                  55                  60
Glu Met Val Ser Lys Glu Ser Glu Arg Leu Ser Ile Thr Lys Ser Ala
65                  70                  75                  80
Cys Gly Arg Asn Gly Lys Gln Phe Cys Ser Thr Leu Thr Leu Asn Thr
                85                  90                  95
Ala Gln Ala Asn His Thr Gly Phe Tyr Ser Cys Lys Tyr Leu Ala Val
            100                 105                 110
Pro Thr Ser Lys Lys Lys Glu Thr Glu Ser Ala Ile Tyr Ile Phe Ile
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Ser Asp Thr Gly Arg Pro Phe Val Glu Met Tyr Ser Glu Ile Pro Glu
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Ile Ile His Met Thr Glu Gly Arg Glu Leu Val Ile Pro Cys Arg Val
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Thr Ser Pro Asn Ile Thr Val Thr Leu Lys Lys Phe Pro Leu Asp Thr
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Leu Ile Pro Asp Gly Lys Arg Ile Ile Trp Asp Ser Arg Lys Gly Phe
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Ile Ile Ser Asn Ala Thr Tyr Lys Glu Ile Gly Leu Leu Thr Cys Glu
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Ala Thr Val Asn Gly His Leu Tyr Lys Thr Asn Tyr Leu Thr His Arg
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Gln Thr Asn Thr Ile Ile Asp Val Gln Ile Ser Thr Pro Arg Pro Val
225                 230                 235                 240
Lys Leu Leu Arg Gly His Thr Leu Val Leu Asn Cys Thr Ala Thr Thr
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Pro Leu Asn Thr Arg Val Gln Met Thr Trp Ser Tyr Pro Asp Glu Lys
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Asn Lys Arg Ala Ser Val Arg Arg Arg Ile Asp Gln Ser Asn Ser His
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Ala Asn Ile Phe Tyr Ser Val Leu Thr Ile Asp Lys Met Gln Asn Lys
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Asp Lys Gly Leu Tyr Thr Cys Arg Val Arg Ser Gly Pro Ser Phe Lys
305                 310                 315                 320
Ser Val Asn Thr Ser Val His Ile Tyr Asp Lys Ala Phe Ile Thr Val
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Lys His Arg Lys Gln Gln Val Leu Glu Thr Val Ala Gly Lys Arg Ser
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Tyr Arg Leu Ser Met Lys Val Lys Ala Phe Pro Ser Pro Glu Val Val
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Trp Leu Lys Asp Gly Leu Pro Ala Thr Glu Lys Ser Ala Arg Tyr Leu
    370                 375                 380
Thr Arg Gly Tyr Ser Leu Ile Ile Lys Asp Val Thr Glu Glu Asp Ala
385                 390                 395                 400
Gly Asn Tyr Thr Ile Leu Leu Ser Ile Lys Gln Ser Asn Val Phe Lys
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Asn Leu Thr Ala Thr Leu Ile Val Asn Val Lys Pro Gln Ile Tyr Glu
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Lys Ala Val Ser Ser Phe Pro Asp Pro Ala Leu Tyr Pro Leu Gly Ser
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Arg Gln Ile Leu Thr Cys Thr Ala Tyr Gly Ile Pro Gln Pro Thr Ile
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Lys Trp Phe Trp His Pro Cys Asn His Asn His Ser Glu Ala Arg Cys
465                 470                 475                 480
Asp Phe Cys Ser Asn Asn Glu Glu Ser Phe Ile Leu Asp Ala Asp Ser
                485                 490                 495
Asn Met Gly Asn Arg Ile Glu Ser Ile Thr Gln Arg Met Ala Ile Ile
            500                 505                 510
Glu Gly Lys Asn Lys Met Ala Ser Thr Leu Val Val Ala Asp Ser Arg
        515                 520                 525
Ile Ser Gly Ile Tyr Ile Cys Ile Ala Ser Asn Lys Val Gly Thr Val
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Gly Arg Asn Ile Ser Phe Tyr Ile Thr Asp Val Pro Asn Gly Phe His
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Val Asn Leu Glu Lys Met Pro Thr Glu Gly Glu Asp Leu Lys Leu Ser
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Cys Thr Val Asn Lys Phe Leu Tyr Arg Asp Val Thr Trp Ile Leu Leu
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Arg Thr Val Asn Asn Arg Thr Met His Tyr Ser Ile Ser Lys Gln Lys
        595                 600                 605
Met Ala Ile Thr Lys Glu His Ser Ile Thr Leu Asn Leu Thr Ile Met
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Asn Val Ser Leu Gln Asp Ser Gly Thr Tyr Ala Cys Arg Ala Arg Asn
625                 630                 635                 640
Val Tyr Thr Gly Glu Glu Ile Leu Gln Lys Lys Glu Ile Thr Ile Arg
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Asp Gln Glu Ala Pro Tyr Leu Leu Arg Asn Leu Ser Asp His Thr Val
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Ala Ile Ser Ser Ser Thr Thr Leu Asp Cys His Ala Asn Gly Val Pro
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Glu Pro Gln Ile Thr Trp Phe Lys Asn Asn His Lys Ile Gln Gln Glu
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Pro Gly Ile Ile Leu Gly Pro Gly Ser Ser Thr Leu Phe Ile Glu Arg
705                 710                 715                 720
Val Thr Glu Glu Asp Glu Gly Val Tyr His Cys Lys Ala Thr Asn Gln
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Lys Gly Ser Val Glu Ser Ser Ala Tyr Leu Thr Val Gln Gly Thr Ser
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Asp Lys Ser Asn Leu Glu Leu Ile Thr Leu Thr Cys Thr Cys Val Ala
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Pro Asp Glu Val Pro Leu Asp Glu Gln Cys Glu Arg Leu Pro Tyr Asp
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Ala Ser Lys Trp Glu Phe Ala Arg Glu Arg Leu Lys Leu Gly Lys Ser
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Leu Gly Arg Gly Ala Phe Gly Lys Val Val Gln Ala Ser Ala Phe Gly
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Ile Lys Lys Ser Pro Thr Cys Arg Thr Val Ala Val Lys Met Leu Lys
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Glu Gly Ala Thr Ala Ser Glu Tyr Lys Ala Leu Met Thr Glu Leu Lys
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Ile Leu Thr His Ile Gly His His Leu Asn Val Val Asn Leu Leu Gly
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Phe Leu Asn Lys Asp Ala Ala Leu His Met Glu Pro Lys Lys Glu Lys
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Thr Ser Ser Glu Ser Phe Ala Ser Ser Gly Phe Gln Glu Asp Lys Ser
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Pro Ile Thr Met Glu Asp Leu Ile Ser Tyr Ser Phe Gln Val Ala Arg
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Gly Met Glu Phe Leu Ser Ser Arg Lys Cys Ile His Arg Asp Leu Ala
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